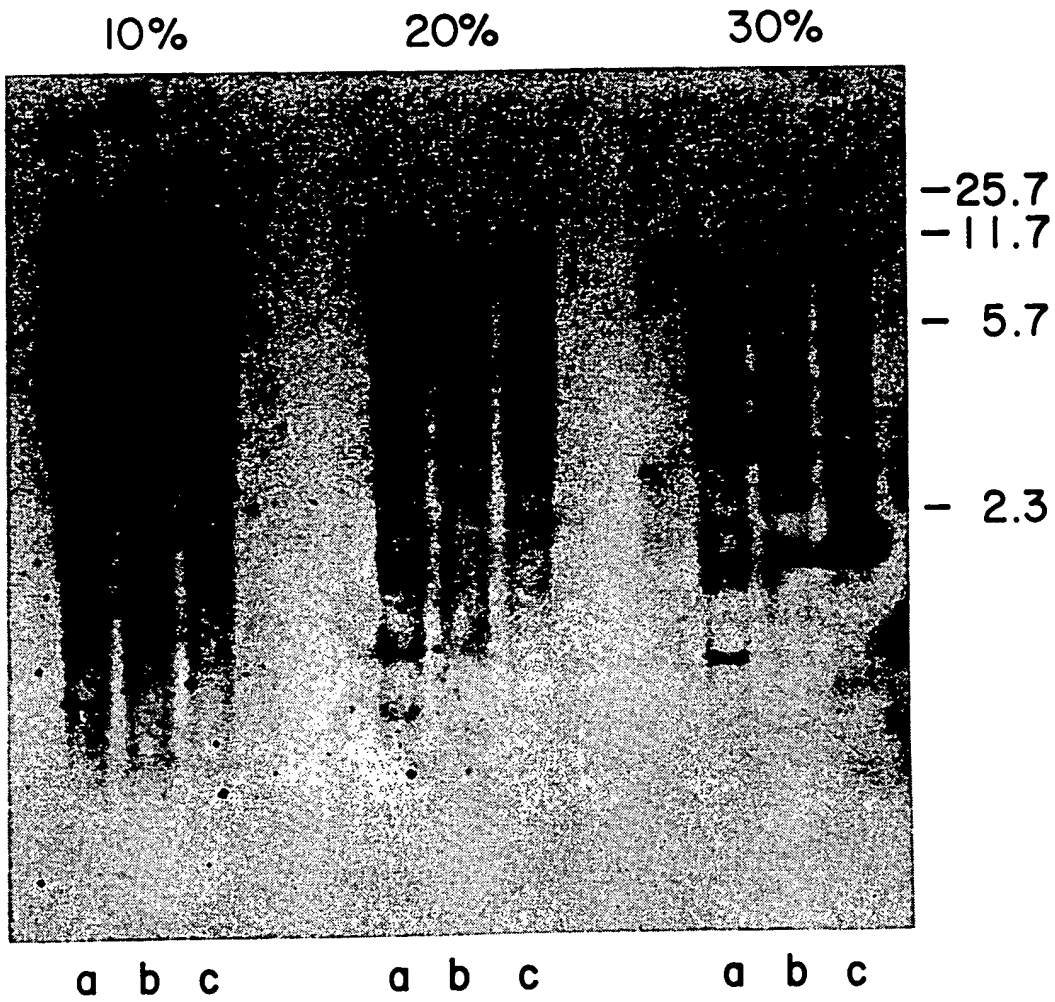
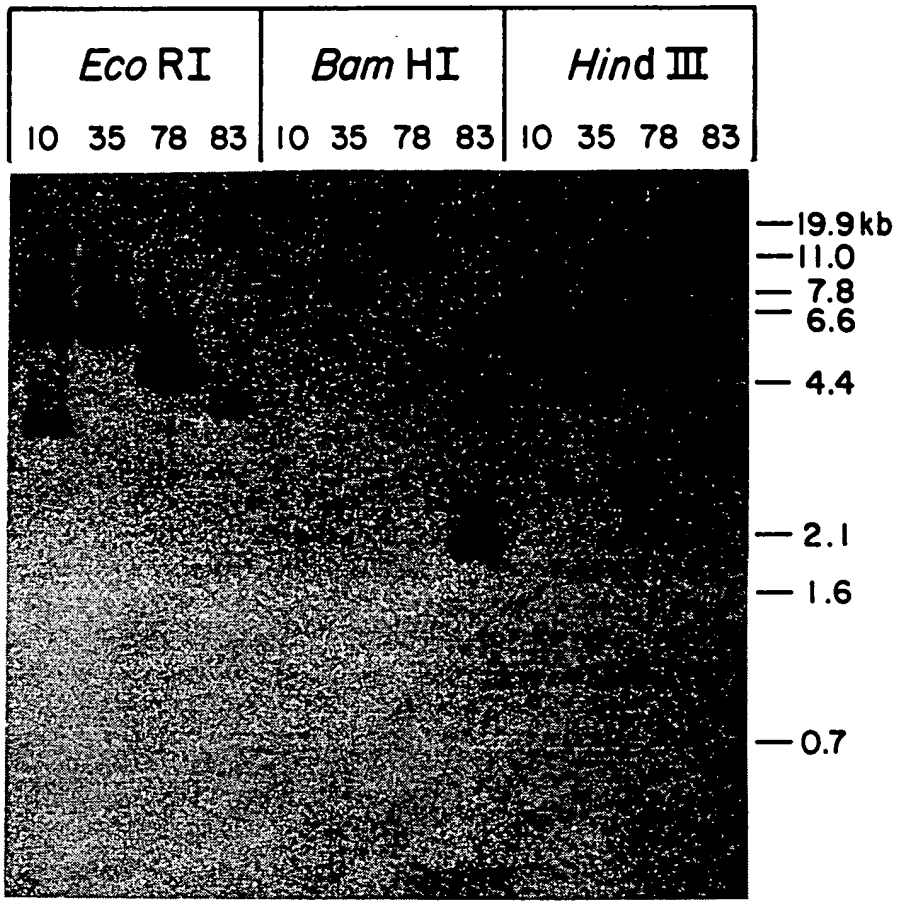


Fig. 13


Eco RI
Bam HI
Hind III
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10 35 78 83
10 35 78 83
19.9kb
11.0
7.8
6.6
4.4
2.1
1.6
0.7

Fig. 8

```
GGATCCACAGCATAAATGTGTTGTCACAATTTCACGGTGGGGGTAATTAGGAAAAAAAAAATCTCAGAAGAACTGTCAATAGGGGAAGGGGGGGCAATAATGAAAACAACGTTTGCGAA
                                                  50                                                 100

ATGCTGTCCTAACCCATTTGAAGAGTACAAACTGAAAAACAAAAACAAAAGTAGAAAGCAAGAGGGAACTTTCAGAAAATGGAAACCATGGACTCCTATTTAAGACACAGACCTGAAGG
                        150                                                 200

                                                                                 S1                                      S10
                                                                                 met ala pro ala trp ser leu leu leu ala
AAGGTCTTCAGAGAACCTAGAAAGCAGGTTCACAGAGTCACCCACCGCCCCAGGCCACAAGCATCTTCAAGGTCCCCG  ATG GCC CCA GCC TGG TCC CTC CTC CTG GCT
          250                                                 300

                                        S20       S23  1                                   10
leu leu leu leu ser cys asn ala ile cys ser leu gly CYS HIS LEU PRO HIS SER HIS SER LEU ALA LYS ARG ARG VAL LEU THR LEU
CTG CTG CTG CTC AGC TGC AAC GCC ATC TGC TCT CTG GGC TGC CAC CTG CCT CAC TCC CAC AGC CTG GCC AAG AGG AGA GTC CTG ACA CTC
 350                                                            400

        20                                      30                                      40
LEU ARG GLN LEU ARG ARG VAL SER PRO SER SER CYS LEU GLN ASP ARG ASN ASP PHE ALA PHE PRO GLN GLU ALA LEU GLY GLY SER GLN
CTG CGA CAA CTG AGG AGG GTC TCC CCT TCC TCC TGC CTG CAG GAC AGA AAT GAC TTC GCA TTC CCC CAG GAG GCG CTG GGT GGC AGC CAG
               450                                                            500

        50                                      60                                      70
LEU GLN LYS ALA GLN ALA ILE SER VAL LEU HIS GLU VAL THR GLN HIS THR PHE GLN LEU PHE SER THR GLU GLY SER ALA ALA VAL TRP
TTG CAG AAG GCT CAA GCC ATC TCT GTA CTC CAC GAG GTG ACC CAA CAC ACC TTC CAG CTT TTC AGC ACA GAG GGC TCG GCC GCT GTG TGG
                         550                                                            600

        80                                      90                                      100
ASP GLU SER LEU LEU ASP LYS LEU ARG THR ALA LEU ASP GLN GLN LEU THR ASP LEU GLN ALA CYS LEU ARG GLN GLU GLU GLY LEU PRO
GAT GAG AGC CTC CTG GAC AAG CTC CGC ACT GCA CTG GAT CAG CAG CTC ACT GAC CTG CAA GCC TGT CTG AGG CAG GAG GAG GGG CTG CCA
                                         650                                                            700

        110                                     120                                     130
GLY ALA PRO LEU LEU LYS GLU ASP SER SER LEU ALA VAL ARG LYS TYR PHE HIS ARG LEU THR LEU TYR LEU GLN GLU LYS ARG HIS SER
GGG GCT CCC CTG CTC AAG GAG GAC TCC AGC CTG GCT GTG AGG AAA TAC TTC CAC AGA CTC ACT CTC TAT CTG CAA GAG AAG AGA CAC AGC
                                                    750

        140                                     150                                     160                     166Stop
PRO CYS ALA TRP GLU VAL VAL ARG ALA GLN VAL MET ARG ALA PHE SER SER SER THR ASN LEU GLN GLU ARG PHE ARG ARG LYS ASP OP
CCT TGT GCC TGG GAG GTT GTC AGA GCA CAA GTC ATG AGA GCC TTC TCT TCC TCA ACA AAC TTG CAG GAG AGA TTC AGG AGA AAG GAC TGA
 800                                                            850

CACACACCTGGTTCAACACGGAAATGATTCTCACGGACCAACAGACCACACTTCCTCCTGCGCTGCCATGTGGAAGACTCATTTCTGCTGTCATCAGGCACTGAACTGAATCAATTTGTT
         900                                                 950                                                 1000

AAATGATTTCAGGTATATTATGTGACATCATGATCTACTCTACAGGCACTACTCTGTCCCAGATACTCAAGCTAATCCATCTACTTATTTATCTATTTGGTATTTATTTATCTAATTTAA
                                        1050                                                1100

TATTTATTTATCTATATATAAAGAATTAAATTATTTTGTTCATATAATTATGTATGTATAATTAATGGAAAAATATATTTTGTATTTAGTCAATTTATGAGTTTTCTTCATTCATTAAAC
                  1150                                                1200

CTTACTATAAAAATCTTCCTTTGTTTTTCTTTAAAAAAGAAACATGAAGACTGAATATGCAACTTGATTAAAGAATGCATTTTTATAATTCCTTCACCCATTTTTGTGATTTGCACATTA
1250                                             1300                                                1350

CAAATGGGGATTTTGGGGGGGATTTTCTGACCGGAACTTGGAAGCGACGAACCTGAAAGAAGGACACTCAGACAGTCTCTTGCAAGGACTGACAAGTTTATTTC
                      1400                                                1450
```

F I G U R E ~~3a~~ 15A

BoIFN-α2

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TAACCCACTGGAGAGTGCAAACTGAAAAGCAAAAACAAAAGTAGAAAATAAGAGGGAACTTTCACAAAGTGGAAACCAT

GGGCTCCTATTTAAGACACAGGCCTGAAGGAAGGTCTTCAGAGAATCTAGAGAGCAGGTTCACAGAGTCACCCACTGCC

                                S1                                      S10
                                met ala pro ala trp ser phe leu leu ala leu leu
CCAGGGCAGAAGCATCTGCAAGGTCCCCG   ATG GCC CCA GCC TGG TCC TTC CTC CTG GCC CTG CTG

                              S20         S23   1
leu leu ser cys asn ala ile cys ser leu gly cys his leu pro his thr his ser leu
CTG CTC AGC TGC AAC GCC ATC TGC TCT TTG GGT TGC CAC CTG CCT CAC ACC CAC AGC CTG

 10                                          20
pro asn arg arg val leu thr leu leu arg gln leu arg arg val ser pro ser ser cys
CCC AAC AGG AGG GTC CTG ACA CTC CTG CGA CAA CTG AGG AGG GTC TCC CCT TCC TCC TGC

 30                                          40
leu gln asp arg asn asp phe ala phe pro gln glu ala leu gly gly ser gln leu gln
CTG CAG GAC AGA AAT GAC TTT GCA TTC CCC CAG GAG GCG CTG GGT GGC AGC CAG TTG CAG

 50                                          60
lys ala gln ala ile ser val leu his glu val thr gln his thr phe gln leu phe ser
AAG GCT CAA GCC ATC TCT GTG CTC CAC GAG GTG ACC CAG CAC ACC TTC CAG CTC TTC AGC

 70                                          80
thr glu gly ser ala ala val trp asp gln ser leu leu asp lys leu arg ala ala leu
ACA GAG GGC TCG GCC GCT GTG TGG GAC CAG AGC CTC CTG GAC AAG CTC CGA GCT GCA CTG

 90                                         100
asp gln gln leu thr asp leu gln ala cys leu arg gln glu glu gly leu arg gly ala
GAT CAG CAG CTC ACT GAC CTG CAA GCC TGT CTG AGG CAG GAG GAG GGG CTG CGA GGG GCT

110                                         120
pro leu leu lys glu asp ala ser leu ala val arg lys tyr phe his arg leu thr leu
CCC CTG CTC AAG GAG GAT GCC AGC CTG GCT GTG AGG AAA TAC TTC CAC AGA CTC ACT CTC

130                                         140
tyr leu gln glu lys arg his ser pro cys ala trp glu val val arg ala glu val met
TAT CTG CAA GAG AAG AGA CAC AGC CCT TGT GCC TGG GAG GTT GTC AGA GCA GAA GTC ATG

150                                         160                     166
arg ala phe ser ser ser thr asn leu gln glu lys phe arg arg lys asp OP
AGA GCC TTC TCT TCT TCA ACA AAC TTG CAG GAG AAA TTC AGG AGA AAG GAC TGA CACACA

CCTGGTTCAACACGGAAATGATTCTCATGGACCAACAGACCACACTTCCTCCTGCACTGCCATGTGGAAGACTCTCAT

TTCTGCTGTCATTGCACCCTGAAATGAATCAATATGTCAAATGATTTCTGGAATATTAAGTAACATCATGTTCTACTC

TATAGGCAAAACAGATGCCGAAGCTCATCTATCTACATATTTAACTACTTGGACATTTATTTATTTATTTTAATATTT

ATTTAACTATTTATAAATATTTAAATTATTTTGTTGATAAAGTATTATGTATGTACATTTAGGGGAAAATGTATATTT

TGTATTTAGTCAGTTTATGATTTTTCTTCCTTTATTAAATTTTTACTGTAAAAGACTTACTTTGTTTTTTCGTTAAAA

CAGAGCCACCAAGCCTGAATGGCAGCTTGATTAAAAATTGCATTTTATGATTCCTTGAGCCCTTTTTAGGATCTGCAT

GTTAGAAGTAAAAATACTCTAGCTCTAGCTATGTTTTTTGTTGCTCTGAGGACCTTGAAGGGAACATAACCACTCCAG

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GATTTGATGAATTC
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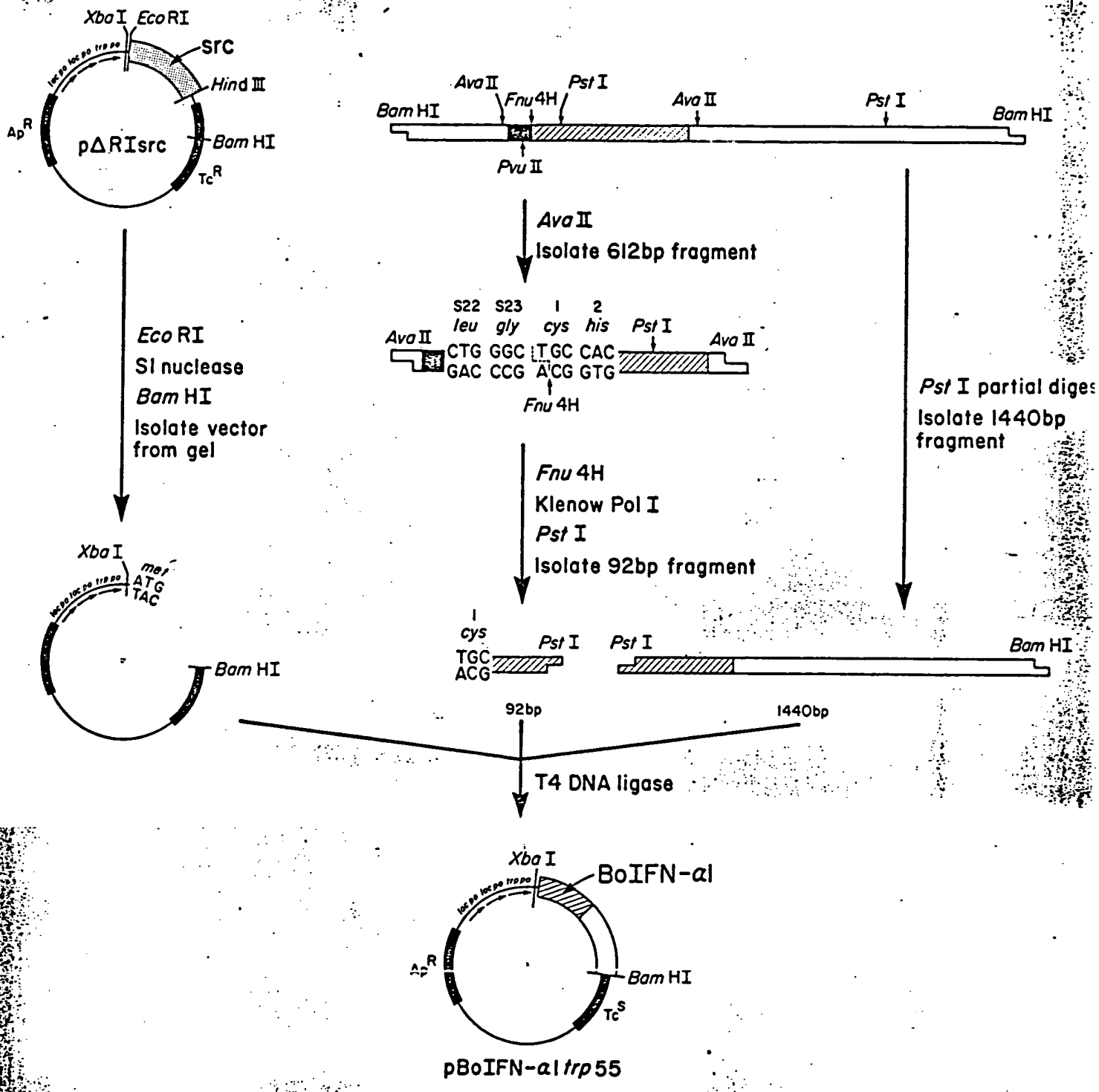
158

FIGURE 5b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Hind III
Ap^R
pΔRIsrc
Bam HI
Tc^R
Ava II
Fnu 4H
Pst I
Ava II
Pst I
Bam HI
Bam HI
Pvu II
Ava II
Isolate 612bp fragment
S22 S23 1 2
leu gly cys his
Pst I
Ava II
Ava II
CTG GGC TGC CAC
GAC CCG ACG GTG
Fnu 4H
Eco RI
S1 nuclease
Bam HI
Isolate vector
from gel
Pst I partial diges
Isolate 1440bp
fragment
Fnu 4H
Klenow Pol I
Pst I
Isolate 92bp fragment
Xba I
met
ATG
TAC
Bam HI
1
cys
TGC
ACG
Pst I
Pst I
Bam HI
92bp
1440bp
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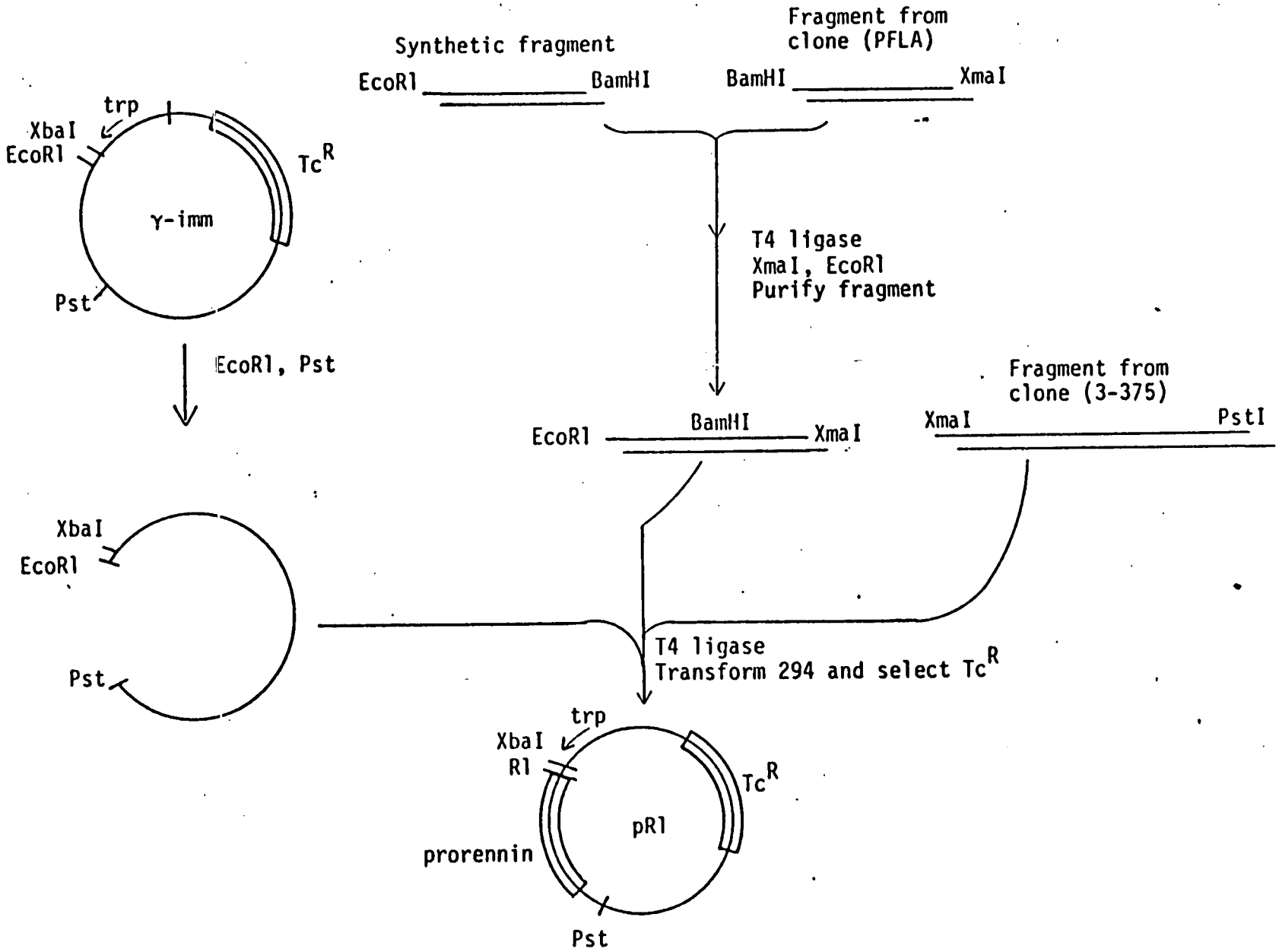
Xba I
BoIFN-α1
Ap^R
Bam HI
Tc^S
pBoIFN-α1trp55

FIGURE 16

Figure 17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EcoRl
BamHI
Fragment from clone (PFLA)
BamHI
XmaI
trp
XbaI
EcoRl
Tc^R
γ-imm
Pst
T4 ligase
XmaI, EcoRl
Purify fragment
EcoRl, Pst
Fragment from clone (3-375)
XmaI
PstI
EcoRl
BamHI
XmaI
XbaI
EcoRl
Pst
T4 ligase
Transform 294 and select Tc^R
trp
XbaI
Rl
Tc^R
pRl
prorennin
Pst